

SEQUENCE LISTING

<110> Japan Science and Technology Corporation

<120> Therapeutic drug containing drug components expressed and fused
with proteins composing nano-particles

<130> P023P01

<150> JP 2002-097280

<151> 2002-3-29

<160> 20

<170> PatentIn Ver. 2.1

<210> 1

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Artificially
Synthesized Sequence

<400> 1

ccggtatctt atcgtcgtca tccttgtaat caatat

36

<210> 2

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Artificially
Synthesized Sequence

<400> 2

atatattgat tacaaggatg acgacgataa gata

34

<210> 3

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Artificially
Synthesized Primer Sequence

<400> 3

ataccggtgg gctgtgatct gcctcaga

28

<210> 4

<211> 28

<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Artificially
Synthesized Primer Sequence

<400> 4
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28

<210> 5
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<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Artificially
Synthesized Primer Sequence

<400> 5
gaaccggtga gctacaactt gcttggatt

29

<210> 6
<211> 30
<212> DNA
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<220>

<223> Description of Artificial Sequence:Artificially
Synthesized Primer Sequence

<400> 6
atgcggccgc tcagtttcgg aggtaacctg

30

<210> 7
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<212> DNA
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<223> Description of Artificial Sequence:Artificially
Synthesized Primer Sequence

<400> 7
gcaccgtac aaaggaaaag aagaaata

28

<210> 8
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<212> DNA
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<220>

<223> Description of Artificial Sequence:Artificially

Synthesized Primer Sequence

<400> 8
ttgcggccgc tatgactgtg gtaccttat 29

<210> 9
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<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Artificially
Synthesized Primer Sequence

<400> 9
ctgtcgaaat ccacgagggg aagaa 25

<210> 10
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Artificially
Synthesized Primer Sequence

<400> 10
ttcttccctt cgtggatttc gacag 25

<210> 11
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Artificially
Synthesized Primer Sequence

<400> 11
tttcccttct cgtgacttga aagat 25

<210> 12
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<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Artificially
Synthesized Primer Sequence

<400> 12
atctttcaag tcacgagaag ggaaa 25

<210> 13
<211> 2013
<212> DNA
<213> Artificial Sequence

<220>
<221> CDS
<222> (23)..(1999)

<220>
<223> Description of Artificial Sequence:GFP gene fused with HBsAg L protein gene

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Met Arg Ser Leu Leu Ile Leu Val Leu Cys
1 5 10

ttc ttg cca ttg gct gct ttg ggt aag gtt cga caa ggc atg ggg acg 100
Phe Leu Pro Leu Ala Ala Leu Gly Lys Val Arg Gln Gly Met Gly Thr
15 20 25

aat ctt tct gtt ccc aat cct ctg gga ttc ttt ccc gat cac cag ttg 148
Asn Leu Ser Val Pro Asn Pro Leu Gly Phe Phe Pro Asp His Gln Leu
30 35 40

gac cct gcg ttc gga gcc aac tca aac aat cca gat tgg gac ttc aac 196
Asp Pro Ala Phe Gly Ala Asn Ser Asn Asn Pro Asp Trp Asp Phe Asn
45 50 55

ccc aac aag gat caa tgg cca gag gca aat cag gta gga gcg gga gca 244
Pro Asn Lys Asp Gln Trp Pro Glu Ala Asn Gln Val Gly Ala Gly Ala
60 65 70

ttc ggg cca ggg ttc acc cca cca cac ggc ggt ctt ttg ggg tgg agc 292
Phe Gly Pro Gly Phe Thr Pro Pro His Gly Gly Leu Leu Gly Trp Ser
75 80 85 90

cct cag gct cag ggc ata ttg aca aca gtg cca gca gca cct cct cct 340
Pro Gln Ala Gln Gly Ile Leu Thr Thr Val Pro Ala Ala Pro Pro Pro
95 100 105

gcc tcc acc aat cgg cag tca gga aga cag cct act ccc atc tct cca 388
Ala Ser Thr Asn Arg Gln Ser Gly Arg Gln Pro Thr Pro Ile Ser Pro
110 115 120

cct cta aga gac agt cat cct cag gcc atg cag tgg aat tcc aca aca 436
Pro Leu Arg Asp Ser His Pro Gln Ala Met Gln Trp Asn Ser Thr Thr
125 130 135

ttc cac caa gct ctg cta gat ccc aga gtg agg ggc cta tat ttt cct 484
Phe His Gln Ala Leu Leu Asp Pro Arg Val Arg Gly Leu Tyr Phe Pro
140 145 150

gct ggt ggc tcc agt tcc gga aca gta aac cct gtt ccg act act gcc 532
Ala Gly Gly Ser Ser Ser Gly Thr Val Asn Pro Val Pro Thr Thr Ala

155	160	165	170	
tca ccc ata tct ggg gac cct gca ccg aac atg gag aac aca aca tca				580
Ser Pro Ile Ser Gly Asp Pro Ala Pro Asn Met Glu Asn Thr Thr Ser				
	175	180	185	
gga ttc cta gga ccc ctg ctc gtg tta cag gcg ggg ttt ttc ttg ttg				628
Gly Phe Leu Gly Pro Leu Leu Val Leu Gln Ala Gly Phe Phe Leu Leu				
	190	195	200	
aca aga atc ctc aca ata cca cag agt cta gac tcg tgg tgg act tct				676
Thr Arg Ile Leu Thr Ile Pro Gln Ser Leu Asp Ser Trp Trp Thr Ser				
	205	210	215	
ctc aat ttt cta ggg gga gca ccc acg tgt cct ggc caa aat tcg cag				724
Leu Asn Phe Leu Gly Gly Ala Pro Thr Cys Pro Gly Gln Asn Ser Gln				
	220	225	230	
tcc cca acc tcc aat cac tca cca acc tct tgt cct cca att tgt cct				772
Ser Pro Thr Ser Asn His Ser Pro Thr Ser Cys Pro Pro Ile Cys Pro				
	235	240	245	250
ggc tat cgc tgg atg tgt ctg cgg cgt ttt atc ata ttc ctc ttc atc				820
Gly Tyr Arg Trp Met Cys Leu Arg Arg Phe Ile Ile Phe Leu Phe Ile				
	255	260	265	
ctg ctg cta tgc ctc atc ttc ttg ttg gtt ctt ctg gac tac caa ggt				868
Leu Leu Leu Cys Leu Ile Phe Leu Leu Val Leu Leu Asp Tyr Gln Gly				
	270	275	280	
atg ttg ccc gtt tgt cct cta ctt cca gga aca tca acc acc agc acg				916
Met Leu Pro Val Cys Pro Leu Leu Pro Gly Thr Ser Thr Thr Ser Thr				
	285	290	295	
ggg cca tgc aag acc tgc acg att cct gct caa gga acc tct atg ttt				964
Gly Pro Cys Lys Thr Cys Thr Ile Pro Ala Gln Gly Thr Ser Met Phe				
	300	305	310	
ccc tct tgt tgc tgt aca aaa cct tcg gac gga aac tgc act tgt att				1012
Pro Ser Cys Cys Cys Thr Lys Pro Ser Asp Gly Asn Cys Thr Cys Ile				
	315	320	325	330
ccc atc cca tca tcc tgg gct ttc gca aga ttc cta tgg gag tgg gcc				1060
Pro Ile Pro Ser Ser Trp Ala Phe Ala Arg Phe Leu Trp Glu Trp Ala				
	335	340	345	
tca gtc cgt ttc tcc tgg ctc agt tta cta gtg cca ttt gtt cag tgg				1108
Ser Val Arg Phe Ser Trp Leu Ser Leu Leu Val Pro Phe Val Gln Trp				
	350	355	360	
ttc gta ggg ctt tcc ccc act gtt tgg ctt tca gtt ata tgg atg atg				1156
Phe Val Gly Leu Ser Pro Thr Val Trp Leu Ser Val Ile Trp Met Met				
	365	370	375	
tgg tat tgg ggg cca agt ctg tac aac atc ttg agt ccc ttt tta cct				1204
Trp Tyr Trp Gly Pro Ser Leu Tyr Asn Ile Leu Ser Pro Phe Leu Pro				
	380	385	390	

cta tta cca att ttc ttt tgt ctt tgg gta tat att gat tac aag gat	1252
Leu Leu Pro Ile Phe Phe Cys Leu Trp Val Tyr Ile Asp Tyr Lys Asp	
395 400 405 410	
gac gac gat aag ata ccg gtc gcc acc atg gtg agc aag ggc gag gag	1300
Asp Asp Asp Lys Ile Pro Val Ala Thr Met Val Ser Lys Gly Glu Glu	
415 420 425	
ctg ttc acc ggg gtg gtg ccc atc ctg gtc gag ctg gac ggc gac gta	1348
Leu Phe Thr Gly Val Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val	
430 435 440	
aac ggc cac aag ttc agc gtg tcc ggc gag ggc gag ggc gat gcc acc	1396
Asn Gly His Lys Phe Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr	
445 450 455	
tac ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc	1444
Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro	
460 465 470	
gtg ccc tgg ccc acc ctg gtg acc acc ctg acc tac ggc gtg cag tgc	1492
Val Pro Trp Pro Thr Leu Val Thr Thr Leu Thr Tyr Gly Val Gln Cys	
475 480 485 490	
ttc agc cgc tac ccc gac cac atg aag cag cac gac ttc ttc aag tcc	1540
Phe Ser Arg Tyr Pro Asp His Met Lys Gln His Asp Phe Phe Lys Ser	
495 500 505	
gcc atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac	1588
Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp	
510 515 520	
gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc	1636
Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr	
525 530 535	
ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc	1684
Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly	
540 545 550	
aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc	1732
Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val	
555 560 565 570	
tat atc atg gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag	1780
Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys	
575 580 585	
atc cgc cac aac atc gag gac ggc agc gtg cag ctg gcc gac cac tac	1828
Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr	
590 595 600	
cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac	1876
Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn	
605 610 615	

cac tac ctg agc acc cag tcc gcc ctg agc aaa gac ccc aac gag aag 1924
 His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys
 620 625 630

cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act 1972
 Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr
 635 640 645 650

ctc ggc atg gac gag ctg tac aag taa agcggccct cgag 2013
 Leu Gly Met Asp Glu Leu Tyr Lys
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<210> 14

<211> 658

<212> PRT

<213> Artificial Sequence

<223> Description of Artificial Sequence:GFP protein fused with HBsAg L protein

<400> 14

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 20 25 30
 Pro Leu Gly Phe Phe Pro Asp His Gln Leu Asp Pro Ala Phe Gly Ala
 35 40 45
 Asn Ser Asn Asn Pro Asp Trp Asp Phe Asn Pro Asn Lys Asp Gln Trp
 50 55 60
 Pro Glu Ala Asn Gln Val Gly Ala Gly Ala Phe Gly Pro Gly Phe Thr
 65 70 75 80
 Pro Pro His Gly Gly Leu Leu Gly Trp Ser Pro Gln Ala Gln Gly Ile
 85 90 95
 Leu Thr Thr Val Pro Ala Ala Pro Pro Pro Ala Ser Thr Asn Arg Gln
 100 105 110
 Ser Gly Arg Gln Pro Thr Pro Ile Ser Pro Pro Leu Arg Asp Ser His
 115 120 125
 Pro Gln Ala Met Gln Trp Asn Ser Thr Thr Phe His Gln Ala Leu Leu
 130 135 140
 Asp Pro Arg Val Arg Gly Leu Tyr Phe Pro Ala Gly Gly Ser Ser Ser
 145 150 155 160
 Gly Thr Val Asn Pro Val Pro Thr Thr Ala Ser Pro Ile Ser Gly Asp
 165 170 175
 Pro Ala Pro Asn Met Glu Asn Thr Thr Ser Gly Phe Leu Gly Pro Leu
 180 185 190
 Leu Val Leu Gln Ala Gly Phe Phe Leu Leu Thr Arg Ile Leu Thr Ile
 195 200 205
 Pro Gln Ser Leu Asp Ser Trp Trp Thr Ser Leu Asn Phe Leu Gly Gly
 210 215 220
 Ala Pro Thr Cys Pro Gly Gln Asn Ser Gln Ser Pro Thr Ser Asn His
 225 230 235 240
 Ser Pro Thr Ser Cys Pro Pro Ile Cys Pro Gly Tyr Arg Trp Met Cys
 245 250 255
 Leu Arg Arg Phe Ile Ile Phe Leu Phe Ile Leu Leu Leu Cys Leu Ile
 260 265 270
 Phe Leu Leu Val Leu Leu Asp Tyr Gln Gly Met Leu Pro Val Cys Pro
 275 280 285

Leu	Leu	Pro	Gly	Thr	Ser	Thr	Thr	Ser	Thr	Gly	Pro	Cys	Lys	Thr	Cys
290						295					300				
Thr	Ile	Pro	Ala	Gln	Gly	Thr	Ser	Met	Phe	Pro	Ser	Cys	Cys	Cys	Thr
305					310					315					320
Lys	Pro	Ser	Asp	Gly	Asn	Cys	Thr	Cys	Ile	Pro	Ile	Pro	Ser	Ser	Trp
				325					330						335
Ala	Phe	Ala	Arg	Phe	Leu	Trp	Glu	Trp	Ala	Ser	Val	Arg	Phe	Ser	Trp
			340					345					350		
Leu	Ser	Leu	Leu	Val	Pro	Phe	Val	Gln	Trp	Phe	Val	Gly	Leu	Ser	Pro
		355					360					365			
Thr	Val	Trp	Leu	Ser	Val	Ile	Trp	Met	Met	Trp	Tyr	Trp	Gly	Pro	Ser
	370					375						380			
Leu	Tyr	Asn	Ile	Leu	Ser	Pro	Phe	Leu	Pro	Leu	Leu	Pro	Ile	Phe	Phe
385					390					395					400
Cys	Leu	Trp	Val	Tyr	Ile	Asp	Tyr	Lys	Asp	Asp	Asp	Asp	Lys	Ile	Pro
				405					410					415	
Val	Ala	Thr	Met	Val	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val
			420					425					430		
Pro	Ile	Leu	Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	Ser
		435					440					445			
Val	Ser	Gly	Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu
	450					455					460				
Lys	Phe	Ile	Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu
465					470					475					480
Val	Thr	Thr	Leu	Thr	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro	Asp
				485					490					495	
His	Met	Lys	Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr
			500					505					510		
Val	Gln	Glu	Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr
		515					520					525			
Arg	Ala	Glu	Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu
		530				535					540				
Leu	Lys	Gly	Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys
545					550					555					560
Leu	Glu	Tyr	Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	Lys
				565					570					575	
Gln	Lys	Asn	Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	Glu
			580					585					590		
Asp	Gly	Ser	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	Ile
		595					600					605			
Gly	Asp	Gly	Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr	Gln
	610					615					620				
Ser	Ala	Leu	Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val	Leu
625					630					635					640
Leu	Glu	Phe	Val	Thr	Ala	Ala	Gly	Ile	Thr	Leu	Gly	Met	Asp	Glu	Leu
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Tyr Lys

<210> 15
 <211> 1803
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> CDS

<222> (23)..(1795)

<220>

<223> Description of Artificial Sequence:IFNfÖ gene fused with HBsAg L protein gene

<400> 15

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ttc ttg cca ttg gct gct ttg ggt aag gtt cga caa ggc atg ggg acg 100
Phe Leu Pro Leu Ala Ala Leu Gly Lys Val Arg Gln Gly Met Gly Thr
                      15             20             25

aat ctt tct gtt ccc aat cct ctg gga ttc ttt ccc gat cac cag ttg 148
Asn Leu Ser Val Pro Asn Pro Leu Gly Phe Phe Pro Asp His Gln Leu
                      30             35             40

gac cct gcg ttc gga gcc aac tca aac aat cca gat tgg gac ttc aac 196
Asp Pro Ala Phe Gly Ala Asn Ser Asn Asn Pro Asp Trp Asp Phe Asn
                      45             50             55

ccc aac aag gat caa tgg cca gag gca aat cag gta gga gcg gga gca 244
Pro Asn Lys Asp Gln Trp Pro Glu Ala Asn Gln Val Gly Ala Gly Ala
                      60             65             70

ttc ggg cca ggg ttc acc cca cca cac ggc ggt ctt ttg ggg tgg agc 292
Phe Gly Pro Gly Phe Thr Pro Pro His Gly Gly Leu Leu Gly Trp Ser
                      75             80             85             90

cct cag gct cag ggc ata ttg aca aca gtg cca gca gca cct cct cct 340
Pro Gln Ala Gln Gly Ile Leu Thr Thr Val Pro Ala Ala Pro Pro Pro
                      95             100             105

gcc tcc acc aat cgg cag tca gga aga cag cct act ccc atc tct cca 388
Ala Ser Thr Asn Arg Gln Ser Gly Arg Gln Pro Thr Pro Ile Ser Pro
                      110             115             120

cct cta aga gac agt cat cct cag gcc atg cag tgg aat tcc aca aca 436
Pro Leu Arg Asp Ser His Pro Gln Ala Met Gln Trp Asn Ser Thr Thr
                      125             130             135

ttc cac caa gct ctg cta gat ccc aga gtg agg ggc cta tat ttt cct 484
Phe His Gln Ala Leu Leu Asp Pro Arg Val Arg Gly Leu Tyr Phe Pro
                      140             145             150

gct ggt ggc tcc agt tcc gga aca gta aac cct gtt ccg act act gcc 532
Ala Gly Gly Ser Ser Ser Gly Thr Val Asn Pro Val Pro Thr Thr Ala
                      155             160             165             170

tca ccc ata tct ggg gac cct gca ccg aac atg gag aac aca aca tca 580
Ser Pro Ile Ser Gly Asp Pro Ala Pro Asn Met Glu Asn Thr Thr Ser
                      175             180             185

gga ttc cta gga ccc ctg ctg gtg tta cag gcg ggg ttt ttc ttg ttg 628
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Gly	Phe	Leu	Gly	Pro	Leu	Leu	Val	Leu	Gln	Ala	Gly	Phe	Phe	Leu	Leu	
			190					195					200			
aca	aga	atc	ctc	aca	ata	cca	cag	agt	cta	gac	tcg	tgg	tgg	act	tct	676
Thr	Arg	Ile	Leu	Thr	Ile	Pro	Gln	Ser	Leu	Asp	Ser	Trp	Trp	Thr	Ser	
		205					210					215				
ctc	aat	ttt	cta	ggg	gga	gca	ccc	acg	tgt	cct	ggc	caa	aat	tcg	cag	724
Leu	Asn	Phe	Leu	Gly	Gly	Ala	Pro	Thr	Cys	Pro	Gly	Gln	Asn	Ser	Gln	
	220					225					230					
tcc	cca	acc	tcc	aat	cac	tca	cca	acc	tct	tgt	cct	cca	att	tgt	cct	772
Ser	Pro	Thr	Ser	Asn	His	Ser	Pro	Thr	Ser	Cys	Pro	Pro	Ile	Cys	Pro	
235					240					245					250	
ggc	tat	cgc	tgg	atg	tgt	ctg	cgg	cgt	ttt	atc	ata	ttc	ctc	ttc	atc	820
Gly	Tyr	Arg	Trp	Met	Cys	Leu	Arg	Arg	Phe	Ile	Ile	Phe	Leu	Phe	Ile	
				255					260					265		
ctg	ctg	cta	tgc	ctc	atc	ttc	ttg	ttg	gtt	ctt	ctg	gac	tac	caa	ggc	868
Leu	Leu	Leu	Cys	Leu	Ile	Phe	Leu	Leu	Val	Leu	Leu	Asp	Tyr	Gln	Gly	
			270					275					280			
atg	ttg	ccc	gtt	tgt	cct	cta	ctt	cca	gga	aca	tca	acc	acc	agc	acg	916
Met	Leu	Pro	Val	Cys	Pro	Leu	Leu	Pro	Gly	Thr	Ser	Thr	Thr	Ser	Thr	
		285					290					295				
ggg	cca	tgc	aag	acc	tgc	acg	att	cct	gct	caa	gga	acc	tct	atg	ttt	964
Gly	Pro	Cys	Lys	Thr	Cys		Ile	Pro	Ala	Gln	Gly	Thr	Ser	Met	Phe	
	300					305					310					
ccc	tct	tgt	tgc	tgt	aca	aaa	cct	tcg	gac	gga	aac	tgc	act	tgt	att	1012
Pro	Ser	Cys	Cys	Cys	Thr	Lys	Pro	Ser	Asp	Gly	Asn	Cys	Thr	Cys	Ile	
315					320					325					330	
ccc	atc	cca	tca	tcc	tgg	gct	ttc	gca	aga	ttc	cta	tgg	gag	tgg	gcc	1060
Pro	Ile	Pro	Ser	Ser	Trp	Ala	Phe	Ala	Arg	Phe	Leu	Trp	Glu	Trp	Ala	
				335				340						345		
tca	gtc	cgt	ttc	tcc	tgg	ctc	agt	tta	cta	gtg	cca	ttt	gtt	cag	tgg	1108
Ser	Val	Arg	Phe	Ser	Trp	Leu	Ser	Leu	Leu	Val	Pro	Phe	Val	Gln	Trp	
			350					355					360			
ttc	gta	ggg	ctt	tcc	ccc	act	gtt	tgg	ctt	tca	gtt	ata	tgg	atg	atg	1156
Phe	Val	Gly	Leu	Ser	Pro	Thr	Val	Trp	Leu	Ser	Val	Ile	Trp	Met	Met	
		365					370					375				
tgg	tat	tgg	ggg	cca	agt	ctg	tac	aac	atc	ttg	agt	ccc	ttt	tta	cct	1204
Trp	Tyr	Trp	Gly	Pro	Ser	Leu	Tyr	Asn	Ile	Leu	Ser	Pro	Phe	Leu	Pro	
	380					385					390					
cta	tta	cca	att	ttc	ttt	tgt	ctt	tgg	gta	tat	att	gat	tac	aag	gat	1252
Leu	Leu	Pro	Ile	Phe	Phe	Cys	Leu	Trp	Val	Tyr	Ile	Asp	Tyr	Lys	Asp	
395					400					405					410	
gac	gac	gat	aag	ata	ccg	gtg	ggc	tgt	gat	ctg	cct	cag	aac	cat	ggc	1300
Asp	Asp	Asp	Lys	Ile	Pro	Val	Gly	Cys	Asp	Leu	Pro	Gln	Asn	His	Gly	

415										420										425										
cta	ctt	agc	agg	aac	acc	ttg	gtg	ctt	ctg	cac	caa	atg	agg	aga	atc	1348														
Leu	Leu	Ser	Arg	Asn	Thr	Leu	Val	Leu	Leu	His	Gln	Met	Arg	Arg	Ile															
430					435					440																				
tcc	cct	ttc	ttg	tgt	ctc	aag	gac	aga	aga	gac	ttc	agg	ttc	ccc	cag	1396														
Ser	Pro	Phe	Leu	Cys	Leu	Lys	Asp	Arg	Arg	Asp	Phe	Arg	Phe	Pro	Gln															
445					450					455																				
gag	atg	gta	aaa	ggg	agc	cag	ttg	cag	aag	gcc	cat	gtc	atg	tct	gtc	1444														
Glu	Met	Val	Lys	Gly	Ser	Gln	Leu	Gln	Lys	Ala	His	Val	Met	Ser	Val															
460					465					470																				
ctc	cat	gag	atg	ctg	cag	cag	atc	ttc	agc	ctc	ttc	cac	aca	gag	cgc	1492														
Leu	His	Glu	Met	Leu	Gln	Gln	Ile	Phe	Ser	Leu	Phe	His	Thr	Glu	Arg															
475					480					485					490															
tcc	tct	gct	gcc	tgg	aac	atg	acc	ctc	cta	gac	caa	ctc	cac	act	gga	1540														
Ser	Ser	Ala	Ala	Trp	Asn	Met	Thr	Leu	Leu	Asp	Gln	Leu	His	Thr	Gly															
495					500					505																				
ctt	cat	cag	caa	ctg	caa	cac	ctg	gag	acc	tgc	ttg	ctg	cag	gta	gtg	1588														
Leu	His	Gln	Gln	Leu	Gln	His	Leu	Glu	Thr	Cys	Leu	Leu	Gln	Val	Val															
510					515					520																				
gga	gaa	gga	gaa	tct	gct	ggg	gca	att	agc	agc	cct	gca	ctg	acc	ttg	1636														
Gly	Glu	Gly	Glu	Ser	Ala	Gly	Ala	Ile	Ser	Ser	Pro	Ala	Leu	Thr	Leu															
525					530					535																				
agg	agg	tac	ttc	cag	gga	atc	cgt	gtc	tac	ctg	aaa	gag	aag	aaa	tac	1684														
Arg	Arg	Tyr	Phe	Gln	Gly	Ile	Arg	Val	Tyr	Leu	Lys	Glu	Lys	Lys	Tyr															
540					545					550																				
agc	gac	tgt	gcc	tgg	gaa	gtt	gtc	aga	atg	gaa	atc	atg	aaa	tcc	ttg	1732														
Ser	Asp	Cys	Ala	Trp	Glu	Val	Val	Arg	Met	Glu	Ile	Met	Lys	Ser	Leu															
555					560					565					570															
ttc	tta	tca	aca	aac	atg	caa	gaa	aga	ctg	aga	agt	aaa	gat	aga	gac	1780														
Phe	Leu	Ser	Thr	Asn	Met	Gln	Glu	Arg	Leu	Arg	Ser	Lys	Asp	Arg	Asp															
575					580					585																				
ctg	ggc	tca	tct	tga	gcggccgc											1803														
Leu	Gly	Ser	Ser																											
590																														

<210> 16

<211> 590

<212> PRT

<213> Artificial Sequence

<223> Description of Artificial Sequence: IFNfÖ protein fused with HBsAg L protein

<400> 16

Met Arg Ser Leu Leu Ile Leu Val Leu Cys Phe Leu Pro Leu Ala Ala

1

5

10

15

Leu	Gly	Lys	Val	Arg	Gln	Gly	Met	Gly	Thr	Asn	Leu	Ser	Val	Pro	Asn	
			20					25					30			
Pro	Leu	Gly	Phe	Phe	Pro	Asp	His	Gln	Leu	Asp	Pro	Ala	Phe	Gly	Ala	
		35					40					45				
Asn	Ser	Asn	Asn	Pro	Asp	Trp	Asp	Phe	Asn	Pro	Asn	Lys	Asp	Gln	Trp	
	50					55					60					
Pro	Glu	Ala	Asn	Gln	Val	Gly	Ala	Gly	Ala	Phe	Gly	Pro	Gly	Phe	Thr	
65					70					75					80	
Pro	Pro	His	Gly	Gly	Leu	Leu	Gly	Trp	Ser	Pro	Gln	Ala	Gln	Gly	Ile	
				85					90					95		
Leu	Thr	Thr	Val	Pro	Ala	Ala	Pro	Pro	Pro	Ala	Ser	Thr	Asn	Arg	Gln	
			100					105					110			
Ser	Gly	Arg	Gln	Pro	Thr	Pro	Ile	Ser	Pro	Pro	Leu	Arg	Asp	Ser	His	
		115					120					125				
Pro	Gln	Ala	Met	Gln	Trp	Asn	Ser	Thr	Thr	Phe	His	Gln	Ala	Leu	Leu	
	130					135					140					
Asp	Pro	Arg	Val	Arg	Gly	Leu	Tyr	Phe	Pro	Ala	Gly	Gly	Ser	Ser	Ser	
145					150					155					160	
Gly	Thr	Val	Asn	Pro	Val	Pro	Thr	Thr	Ala	Ser	Pro	Ile	Ser	Gly	Asp	
			165						170					175		
Pro	Ala	Pro	Asn	Met	Glu	Asn	Thr	Thr	Ser	Gly	Phe	Leu	Gly	Pro	Leu	
			180					185					190			
Leu	Val	Leu	Gln	Ala	Gly	Phe	Phe	Leu	Leu	Thr	Arg	Ile	Leu	Thr	Ile	
	195						200					205				
Pro	Gln	Ser	Leu	Asp	Ser	Trp	Trp	Thr	Ser	Leu	Asn	Phe	Leu	Gly	Gly	
	210					215					220					
Ala	Pro	Thr	Cys	Pro	Gly	Gln	Asn	Ser	Gln	Ser	Pro	Thr	Ser	Asn	His	
225					230					235					240	
Ser	Pro	Thr	Ser	Cys	Pro	Pro	Ile	Cys	Pro	Gly	Tyr	Arg	Trp	Met	Cys	
			245						250					255		
Leu	Arg	Arg	Phe	Ile	Ile	Phe	Leu	Phe	Ile	Leu	Leu	Leu	Cys	Leu	Ile	
			260					265					270			
Phe	Leu	Leu	Val	Leu	Leu	Asp	Tyr	Gln	Gly	Met	Leu	Pro	Val	Cys	Pro	
	275						280					285				
Leu	Leu	Pro	Gly	Thr	Ser	Thr	Thr	Ser	Thr	Gly	Pro	Cys	Lys	Thr	Cys	
	290					295					300					
Thr	Ile	Pro	Ala	Gln	Gly	Thr	Ser	Met	Phe	Pro	Ser	Cys	Cys	Cys	Thr	
305				310						315					320	
Lys	Pro	Ser	Asp	Gly	Asn	Cys	Thr	Cys	Ile	Pro	Ile	Pro	Ser	Ser	Trp	
			325						330					335		
Ala	Phe	Ala	Arg	Phe	Leu	Trp	Glu	Trp	Ala	Ser	Val	Arg	Phe	Ser	Trp	
		340					345						350			
Leu	Ser	Leu	Leu	Val	Pro	Phe	Val	Gln	Trp	Phe	Val	Gly	Leu	Ser	Pro	
	355						360					365				
Thr	Val	Trp	Leu	Ser	Val	Ile	Trp	Met	Met	Trp	Tyr	Trp	Gly	Pro	Ser	
	370					375					380					
Leu	Tyr	Asn	Ile	Leu	Ser	Pro	Phe	Leu	Pro	Leu	Leu	Pro	Ile	Phe	Phe	
385					390					395					400	
Cys	Leu	Trp	Val	Tyr	Ile	Asp	Tyr	Lys	Asp	Asp	Asp	Asp	Lys	Ile	Pro	
			405						410					415		
Val	Gly	Cys	Asp	Leu	Pro	Gln	Asn	His	Gly	Leu	Leu	Ser	Arg	Asn	Thr	
			420					425					430			
Leu	Val	Leu	Leu	His	Gln	Met	Arg	Arg	Ile	Ser	Pro	Phe	Leu	Cys	Leu	
	435						440					445				
Lys	Asp	Arg	Arg	Asp	Phe	Arg	Phe	Pro	Gln	Glu	Met	Val	Lys	Gly	Ser	
	450					455					460					
Gln	Leu	Gln	Lys	Ala	His	Val	Met	Ser	Val	Leu	His	Glu	Met	Leu	Gln	

Pro	Gln	Ala	Gln	Gly	Ile	Leu	Thr	Thr	Val	Pro	Ala	Ala	Pro	Pro	Pro		
				95					100					105			
gcc	tcc	acc	aat	cgg	cag	tca	gga	aga	cag	cct	act	ccc	atc	tct	cca	388	
Ala	Ser	Thr	Asn	Arg	Gln	Ser	Gly	Arg	Gln	Pro	Thr	Pro	Ile	Ser	Pro		
			110					115					120				
cct	cta	aga	gac	agt	cat	cct	cag	gcc	atg	cag	tgg	aat	tcc	aca	aca	436	
Pro	Leu	Arg	Asp	Ser	His	Pro	Gln	Ala	Met	Gln	Trp	Asn	Ser	Thr	Thr		
			125					130					135				
ttc	cac	caa	gct	ctg	cta	gat	ccc	aga	gtg	agg	ggc	cta	tat	ttt	cct	484	
Phe	His	Gln	Ala	Leu	Leu	Asp	Pro	Arg	Val	Arg	Gly	Leu	Tyr	Phe	Pro		
	140						145				150						
gct	ggt	ggc	tcc	agt	tcc	gga	aca	gta	aac	cct	gtt	ccg	act	act	gcc	532	
Ala	Gly	Gly	Ser	Ser	Ser	Gly	Thr	Val	Asn	Pro	Val	Pro	Thr	Thr	Ala		
	155					160				165					170		
tca	ccc	ata	tct	ggg	gac	cct	gca	ccg	aac	atg	gag	aac	aca	aca	tca	580	
Ser	Pro	Ile	Ser	Gly	Asp	Pro	Ala	Pro	Asn	Met	Glu	Asn	Thr	Thr	Ser		
				175					180						185		
gga	ttc	cta	gga	ccc	ctg	ctc	gtg	tta	cag	gcg	ggg	ttt	ttc	ttg	ttg	628	
Gly	Phe	Leu	Gly	Pro	Leu	Leu	Val	Leu	Gln	Ala	Gly	Phe	Phe	Leu	Leu		
			190					195					200				
aca	aga	atc	ctc	aca	ata	cca	cag	agt	cta	gac	tcg	tgg	tgg	act	tct	676	
Thr	Arg	Ile	Leu	Thr	Ile	Pro	Gln	Ser	Leu	Asp	Ser	Trp	Trp	Thr	Ser		
			205				210					215					
ctc	aat	ttt	cta	ggg	gga	gca	ccc	acg	tgt	cct	ggc	caa	aat	tcg	cag	724	
Leu	Asn	Phe	Leu	Gly	Gly	Ala	Pro	Thr	Cys	Pro	Gly	Gln	Asn	Ser	Gln		
	220					225					230						
tcc	cca	acc	tcc	aat	cac	tca	cca	acc	tct	tgt	cct	cca	att	tgt	cct	772	
Ser	Pro	Thr	Ser	Asn	His	Ser	Pro	Thr	Ser	Cys	Pro	Pro	Ile	Cys	Pro		
	235				240					245					250		
ggc	tat	cgc	tgg	atg	tgt	ctg	cgg	cgt	ttt	atc	ata	ttc	ctc	ttc	atc	820	
Gly	Tyr	Arg	Trp	Met	Cys	Leu	Arg	Arg	Phe	Ile	Ile	Phe	Leu	Phe	Ile		
				255					260					265			
ctg	ctg	cta	tgc	ctc	atc	ttc	ttg	ttg	gtt	ctt	ctg	gac	tac	caa	ggc	868	
Leu	Leu	Leu	Cys	Leu	Ile	Phe	Leu	Leu	Val	Leu	Leu	Asp	Tyr	Gln	Gly		
			270					275					280				
atg	ttg	ccc	gtt	tgt	cct	cta	ctt	cca	gga	aca	tca	acc	acc	agc	acg	916	
Met	Leu	Pro	Val	Cys	Pro	Leu	Leu	Pro	Gly	Thr	Ser	Thr	Thr	Ser	Thr		
			285				290					295					
ggg	cca	tgc	aag	acc	tgc	acg	att	cct	gct	caa	gga	acc	tct	atg	ttt	964	
Gly	Pro	Cys	Lys	Thr	Cys	Thr	Ile	Pro	Ala	Gln	Gly	Thr	Ser	Met	Phe		
	300					305					310						
ccc	tct	tgt	tgc	tgt	aca	aaa	cct	tcg	gac	gga	aac	tgc	act	tgt	att	1012	
Pro	Ser	Cys	Cys	Cys	Thr	Lys	Pro	Ser	Asp	Gly	Asn	Cys	Thr	Cys	Ile		

315	320	325	330	
ccc atc cca tca tcc tgg gct ttc gca aga ttc cta tgg gag tgg gcc				1060
Pro Ile Pro Ser Ser Trp Ala Phe Ala Arg Phe Leu Trp Glu Trp Ala	335	340	345	
tca gtc cgt ttc tcc tgg ctc agt tta cta gtg cca ttt gtt cag tgg				1108
Ser Val Arg Phe Ser Trp Leu Ser Leu Leu Val Pro Phe Val Gln Trp	350	355	360	
ttc gta ggg ctt tcc ccc act gtt tgg ctt tca gtt ata tgg atg atg				1156
Phe Val Gly Leu Ser Pro Thr Val Trp Leu Ser Val Ile Trp Met Met	365	370	375	
tgg tat tgg ggg cca agt ctg tac aac atc ttg agt ccc ttt tta cct				1204
Trp Tyr Trp Gly Pro Ser Leu Tyr Asn Ile Leu Ser Pro Phe Leu Pro	380	385	390	
cta tta cca att ttc ttt tgt ctt tgg gta tat att gat tac aag gat				1252
Leu Leu Pro Ile Phe Phe Cys Leu Trp Val Tyr Ile Asp Tyr Lys Asp	395	400	405	410
gac gac gat aag ata ccg gtg agc tac aac ttg ctt gga ttc cta caa				1300
Asp Asp Asp Lys Ile Pro Val Ser Tyr Asn Leu Leu Gly Phe Leu Gln	415	420	425	
aga agc agc aat ttt cag tgt cag aag ctc ctg tgg caa ttg aat ggg				1348
Arg Ser Ser Asn Phe Gln Cys Gln Lys Leu Leu Trp Gln Leu Asn Gly	430	435	440	
agg ctt gaa tac tgc ctc aag gac agg atg aac ttt gac atc cct gag				1396
Arg Leu Glu Tyr Cys Leu Lys Asp Arg Met Asn Phe Asp Ile Pro Glu	445	450	455	
gag att aag cag ctg cag cag ttc cag aag gag gac gcc gca ttg acc				1444
Glu Ile Lys Gln Leu Gln Gln Phe Gln Lys Glu Asp Ala Ala Leu Thr	460	465	470	
atc tat gag atg ctc cag aac atc ttt gct att ttc aga caa gat tca				1492
Ile Tyr Glu Met Leu Gln Asn Ile Phe Ala Ile Phe Arg Gln Asp Ser	475	480	485	490
tct agc act ggc tgg aat gag act att gtt gag aac ctc ctg gct aat				1540
Ser Ser Thr Gly Trp Asn Glu Thr Ile Val Glu Asn Leu Leu Ala Asn	495	500	505	
gtc tat cat cag ata aac cat ctg aag aca gtc ctg gaa gaa aaa ctg				1588
Val Tyr His Gln Ile Asn His Leu Lys Thr Val Leu Glu Glu Lys Leu	510	515	520	
gag aaa gaa gat ttc acc agg gga aaa ctc atg agc agt ctg cac ctg				1636
Glu Lys Glu Asp Phe Thr Arg Gly Lys Leu Met Ser Ser Leu His Leu	525	530	535	
aaa aga tat tat ggg agg att ctg cat tac ctg aag gcc aag gag tac				1684
Lys Arg Tyr Tyr Gly Arg Ile Leu His Tyr Leu Lys Ala Lys Glu Tyr	540	545	550	

agt cac tgt gcc tgg acc ata gtc aga gtg gaa atc cta agg aac ttt 1732
 Ser His Cys Ala Trp Thr Ile Val Arg Val Glu Ile Leu Arg Asn Phe
 555 560 565 570

tac ttc att aac aga ctt aca ggt tac ctc cga aac tga gcggccgc 1779
 Tyr Phe Ile Asn Arg Leu Thr Gly Tyr Leu Arg Asn
 575 580

<210> 18

<211> 582

<212> PRT

<213> Artificial Sequence

<223> Description of Artificial Sequence: IFN γ protein fused with HBsAg L protein

<400> 18

Met Arg Ser Leu Leu Ile Leu Val Leu Cys Phe Leu Pro Leu Ala Ala
 1 5 10 15
 Leu Gly Lys Val Arg Gln Gly Met Gly Thr Asn Leu Ser Val Pro Asn
 20 25 30
 Pro Leu Gly Phe Phe Pro Asp His Gln Leu Asp Pro Ala Phe Gly Ala
 35 40 45
 Asn Ser Asn Asn Pro Asp Trp Asp Phe Asn Pro Asn Lys Asp Gln Trp
 50 55 60
 Pro Glu Ala Asn Gln Val Gly Ala Gly Ala Phe Gly Pro Gly Phe Thr
 65 70 75 80
 Pro Pro His Gly Gly Leu Leu Gly Trp Ser Pro Gln Ala Gln Gly Ile
 85 90 95
 Leu Thr Thr Val Pro Ala Ala Pro Pro Pro Ala Ser Thr Asn Arg Gln
 100 105 110
 Ser Gly Arg Gln Pro Thr Pro Ile Ser Pro Pro Leu Arg Asp Ser His
 115 120 125
 Pro Gln Ala Met Gln Trp Asn Ser Thr Thr Phe His Gln Ala Leu Leu
 130 135 140
 Asp Pro Arg Val Arg Gly Leu Tyr Phe Pro Ala Gly Gly Ser Ser Ser
 145 150 155 160
 Gly Thr Val Asn Pro Val Pro Thr Thr Ala Ser Pro Ile Ser Gly Asp
 165 170 175
 Pro Ala Pro Asn Met Glu Asn Thr Thr Ser Gly Phe Leu Gly Pro Leu
 180 185 190
 Leu Val Leu Gln Ala Gly Phe Phe Leu Leu Thr Arg Ile Leu Thr Ile
 195 200 205
 Pro Gln Ser Leu Asp Ser Trp Trp Thr Ser Leu Asn Phe Leu Gly Gly
 210 215 220
 Ala Pro Thr Cys Pro Gly Gln Asn Ser Gln Ser Pro Thr Ser Asn His
 225 230 235 240
 Ser Pro Thr Ser Cys Pro Pro Ile Cys Pro Gly Tyr Arg Trp Met Cys
 245 250 255
 Leu Arg Arg Phe Ile Ile Phe Leu Phe Ile Leu Leu Leu Cys Leu Ile
 260 265 270
 Phe Leu Leu Val Leu Leu Asp Tyr Gln Gly Met Leu Pro Val Cys Pro

275	280	285
Leu Leu Pro Gly Thr Ser Thr Thr Ser Thr Gly Pro Cys Lys Thr Cys		
290	295	300
Thr Ile Pro Ala Gln Gly Thr Ser Met Phe Pro Ser Cys Cys Cys Thr		
305	310	315
Lys Pro Ser Asp Gly Asn Cys Thr Cys Ile Pro Ile Pro Ser Ser Trp		
325	330	335
Ala Phe Ala Arg Phe Leu Trp Glu Trp Ala Ser Val Arg Phe Ser Trp		
340	345	350
Leu Ser Leu Leu Val Pro Phe Val Gln Trp Phe Val Gly Leu Ser Pro		
355	360	365
Thr Val Trp Leu Ser Val Ile Trp Met Met Trp Tyr Trp Gly Pro Ser		
370	375	380
Leu Tyr Asn Ile Leu Ser Pro Phe Leu Pro Leu Leu Pro Ile Phe Phe		
385	390	395
Cys Leu Trp Val Tyr Ile Asp Tyr Lys Asp Asp Asp Asp Lys Ile Pro		
405	410	415
Val Ser Tyr Asn Leu Leu Gly Phe Leu Gln Arg Ser Ser Asn Phe Gln		
420	425	430
Cys Gln Lys Leu Leu Trp Gln Leu Asn Gly Arg Leu Glu Tyr Cys Leu		
435	440	445
Lys Asp Arg Met Asn Phe Asp Ile Pro Glu Glu Ile Lys Gln Leu Gln		
450	455	460
Gln Phe Gln Lys Glu Asp Ala Ala Leu Thr Ile Tyr Glu Met Leu Gln		
465	470	475
Asn Ile Phe Ala Ile Phe Arg Gln Asp Ser Ser Ser Thr Gly Trp Asn		
485	490	495
Glu Thr Ile Val Glu Asn Leu Leu Ala Asn Val Tyr His Gln Ile Asn		
500	505	510
His Leu Lys Thr Val Leu Glu Glu Lys Leu Glu Lys Glu Asp Phe Thr		
515	520	525
Arg Gly Lys Leu Met Ser Ser Leu His Leu Lys Arg Tyr Tyr Gly Arg		
530	535	540
Ile Leu His Tyr Leu Lys Ala Lys Glu Tyr Ser His Cys Ala Trp Thr		
545	550	555
Ile Val Arg Val Glu Ile Leu Arg Asn Phe Tyr Phe Ile Asn Arg Leu		
565	570	575
Thr Gly Tyr Leu Arg Asn		
580		

<210> 19

<211> 3359

<212> DNA

<213> Artificial Sequence

<220>

<221> CDS

<222> (23)..(3352)

<220>

<223> Description of Artificial Sequence:HGF gene fused with HBsAg L protein gene

<400> 19

ctc	gag	gtc	g	agt	ata	aaaa	ca	atg	aga	tct	ttg	ttg	atc	ttg	gtt	ttg	tgt	52
								Met	Arg	Ser	Leu	Leu	Ile	Leu	Val	Leu	Cys	
								1					5				10	
ttc	ttg	cca	ttg	gct	gct	ttg	ggt	aag	gtt	cga	caa	ggc	atg	ggg	acg			100
Phe	Leu	Pro	Leu	Ala	Ala	Leu	Gly	Lys	Val	Arg	Gln	Gly	Met	Gly	Thr			
				15						20				25				
aat	ctt	tct	gtt	ccc	aat	cct	ctg	gga	ttc	ttt	ccc	gat	cac	cag	ttg			148
Asn	Leu	Ser	Val	Pro	Asn	Pro	Leu	Gly	Phe	Phe	Pro	Asp	His	Gln	Leu			
				30				35					40					
gac	cct	gcg	ttc	gga	gcc	aac	tca	aac	aat	cca	gat	tgg	gac	ttc	aac			196
Asp	Pro	Ala	Phe	Gly	Ala	Asn	Ser	Asn	Asn	Pro	Asp	Trp	Asp	Phe	Asn			
		45					50					55						
ccc	aac	aag	gat	caa	tgg	cca	gag	gca	aat	cag	gta	gga	gcg	gga	gca			244
Pro	Asn	Lys	Asp	Gln	Trp	Pro	Glu	Ala	Asn	Gln	Val	Gly	Ala	Gly	Ala			
	60					65					70							
ttc	ggg	cca	ggg	ttc	acc	cca	cca	cac	ggc	ggt	ctt	ttg	ggg	tgg	agc			292
Phe	Gly	Pro	Gly	Phe	Thr	Pro	Pro	His	Gly	Gly	Leu	Leu	Gly	Trp	Ser			
	75				80				85						90			
cct	cag	gct	cag	ggc	ata	ttg	aca	aca	gtg	cca	gca	gca	cct	cct	cct			340
Pro	Gln	Ala	Gln	Gly	Ile	Leu	Thr	Thr	Val	Pro	Ala	Ala	Pro	Pro	Pro			
				95					100					105				
gcc	tcc	acc	aat	cgg	cag	tca	gga	aga	cag	cct	act	ccc	atc	tct	cca			388
Ala	Ser	Thr	Asn	Arg	Gln	Ser	Gly	Arg	Gln	Pro	Thr	Pro	Ile	Ser	Pro			
			110					115					120					
cct	cta	aga	gac	agt	cat	cct	cag	gcc	atg	cag	tgg	aat	tcc	aca	aca			436
Pro	Leu	Arg	Asp	Ser	His	Pro	Gln	Ala	Met	Gln	Trp	Asn	Ser	Thr	Thr			
		125					130					135						
ttc	cac	caa	gct	ctg	cta	gat	ccc	aga	gtg	agg	ggc	cta	tat	ttt	cct			484
Phe	His	Gln	Ala	Leu	Leu	Asp	Pro	Arg	Val	Arg	Gly	Leu	Tyr	Phe	Pro			
	140					145					150							
gct	ggt	ggc	tcc	agt	tcc	gga	aca	gta	aac	cct	gtt	ccg	act	act	gcc			532
Ala	Gly	Gly	Ser	Ser	Ser	Gly	Thr	Val	Asn	Pro	Val	Pro	Thr	Thr	Ala			
	155				160				165						170			
tca	ccc	ata	tct	ggg	gac	cct	gca	ccg	aac	atg	gag	aac	aca	aca	tca			580
Ser	Pro	Ile	Ser	Gly	Asp	Pro	Ala	Pro	Asn	Met	Glu	Asn	Thr	Thr	Ser			
				175					180					185				
gga	ttc	cta	gga	ccc	ctg	ctc	gtg	tta	cag	gcg	ggg	ttt	ttc	ttg	ttg			628
Gly	Phe	Leu	Gly	Pro	Leu	Leu	Val	Leu	Gln	Ala	Gly	Phe	Phe	Leu	Leu			
				190				195					200					
aca	aga	atc	ctc	aca	ata	cca	cag	agt	cta	gac	tcg	tgg	tgg	act	tct			676
Thr	Arg	Ile	Leu	Thr	Ile	Pro	Gln	Ser	Leu	Asp	Ser	Trp	Trp	Thr	Ser			
		205					210					215						
ctc	aat	ttt	cta	ggg	gga	gca	ccc	acg	tgt	cct	ggc	caa	aat	tcg	cag			724

Leu	Asn	Phe	Leu	Gly	Gly	Ala	Pro	Thr	Cys	Pro	Gly	Gln	Asn	Ser	Gln	
220						225					230					
tcc	cca	acc	tcc	aat	cac	tca	cca	acc	tct	tgt	cct	cca	att	tgt	cct	772
Ser	Pro	Thr	Ser	Asn	His	Ser	Pro	Thr	Ser	Cys	Pro	Pro	Ile	Cys	Pro	
235					240					245					250	
ggc	tat	cgc	tgg	atg	tgt	ctg	cgg	cgt	ttt	atc	ata	ttc	ctc	ttc	atc	820
Gly	Tyr	Arg	Trp	Met	Cys	Leu	Arg	Arg	Phe	Ile	Ile	Phe	Leu	Phe	Ile	
				255					260					265		
ctg	ctg	cta	tgc	ctc	atc	ttc	ttg	ttg	gtt	ctt	ctg	gac	tac	caa	ggc	868
Leu	Leu	Leu	Cys	Leu	Ile	Phe	Leu	Leu	Val	Leu	Leu	Asp	Tyr	Gln	Gly	
			270					275					280			
atg	ttg	ccc	gtt	tgt	cct	cta	ctt	cca	gga	aca	tca	acc	acc	agc	acg	916
Met	Leu	Pro	Val	Cys	Pro	Leu	Leu	Pro	Gly	Thr	Ser	Thr	Thr	Ser	Thr	
		285					290					295				
ggg	cca	tgc	aag	acc	tgc	acg	att	cct	gct	caa	gga	acc	tct	atg	ttt	964
Gly	Pro	Cys	Lys	Thr	Cys	Thr	Ile	Pro	Ala	Gln	Gly	Thr	Ser	Met	Phe	
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ccc	tct	tgt	tgc	tgt	aca	aaa	cct	tcg	gac	gga	aac	tgc	act	tgt	att	1012
Pro	Ser	Cys	Cys	Cys	Thr	Lys	Pro	Ser	Asp	Gly	Asn	Cys	Thr	Cys	Ile	
315					320					325					330	
ccc	atc	cca	tca	tcc	tgg	gct	ttc	gca	aga	ttc	cta	tgg	gag	tgg	gcc	1060
Pro	Ile	Pro	Ser	Ser	Trp	Ala	Phe	Ala	Arg	Phe	Leu	Trp	Glu	Trp	Ala	
				335				340						345		
tca	gtc	cgt	ttc	tcc	tgg	ctc	agt	tta	cta	gtg	cca	ttt	gtt	cag	tgg	1108
Ser	Val	Arg	Phe	Ser	Trp	Leu	Ser	Leu	Leu	Val	Pro	Phe	Val	Gln	Trp	
			350					355					360			
ttc	gta	ggg	ctt	tcc	ccc	act	gtt	tgg	ctt	tca	gtt	ata	tgg	atg	atg	1156
Phe	Val	Gly	Leu	Ser	Pro	Thr	Val	Trp	Leu	Ser	Val	Ile	Trp	Met	Met	
		365					370					375				
tgg	tat	tgg	ggg	cca	agt	ctg	tac	aac	atc	ttg	agt	ccc	ttt	tta	cct	1204
Trp	Tyr	Trp	Gly	Pro	Ser	Leu	Tyr	Asn	Ile	Leu	Ser	Pro	Phe	Leu	Pro	
	380					385					390					
cta	tta	cca	att	ttc	ttt	tgt	ctt	tgg	gta	tat	att	gat	tac	aag	gat	1252
Leu	Leu	Pro	Ile	Phe	Phe	Cys	Leu	Trp	Val	Tyr	Ile	Asp	Tyr	Lys	Asp	
395					400					405					410	
gac	gac	gat	aag	ata	ccg	gta	caa	agg	aaa	aga	aga	aat	aca	att	cat	1300
Asp	Asp	Asp	Lys	Ile	Pro	Val	Gln	Arg	Lys	Arg	Arg	Asn	Thr	Ile	His	
			415					420						425		
gaa	ttc	aaa	aaa	tca	gca	aag	act	acc	cta	atc	aaa	ata	gat	cca	gca	1348
Glu	Phe	Lys	Lys	Ser	Ala	Lys	Thr	Thr	Leu	Ile	Lys	Ile	Asp	Pro	Ala	
			430					435					440			
ctg	aag	ata	aaa	acc	aaa	aaa	gtg	aat	act	gca	gac	caa	tgt	gct	aat	1396
Leu	Lys	Ile	Lys	Thr	Lys	Lys	Val	Asn	Thr	Ala	Asp	Gln	Cys	Ala	Asn	

445	450	455	
aga tgt act agg aat aaa gga ctt cca ttc act tgc aag gct ttt gtt Arg Cys Thr Arg Asn Lys Gly Leu Pro Phe Thr Cys Lys Ala Phe Val 460	465	470	1444
ttt gat aaa gca aga aaa caa tgc ctc tgg ttc ccc ttc aat agc atg Phe Asp Lys Ala Arg Lys Gln Cys Leu Trp Phe Pro Phe Asn Ser Met 475	480	485	1492
tca agt gga gtg aaa aaa gaa ttt ggc cat gaa ttt gac ctc tat gaa Ser Ser Gly Val Lys Lys Glu Phe Gly His Glu Phe Asp Leu Tyr Glu 495	500	505	1540
aac aaa gac tac att aga aac tgc atc att ggt aaa gga cgc agc tac Asn Lys Asp Tyr Ile Arg Asn Cys Ile Ile Gly Lys Gly Arg Ser Tyr 510	515	520	1588
aag gga aca gta tct atc act aag agt ggc atc aaa tgt cag ccc tgg Lys Gly Thr Val Ser Ile Thr Lys Ser Gly Ile Lys Cys Gln Pro Trp 525	530	535	1636
agt tcc atg ata cca cac gaa cac agc tat cgg ggt aaa gac cta cag Ser Ser Met Ile Pro His Glu His Ser Tyr Arg Gly Lys Asp Leu Gln 540	545	550	1684
gaa aac tac tgt cga aat cca cga ggg gaa gaa ggg gga ccc tgg tgt Glu Asn Tyr Cys Arg Asn Pro Arg Gly Glu Glu Gly Gly Pro Trp Cys 555	560	565	1732
ttc aca agc aat cca gag gta cgc tac gaa gtc tgt gac att cct cag Phe Thr Ser Asn Pro Glu Val Arg Tyr Glu Val Cys Asp Ile Pro Gln 575	580	585	1780
tgt tca gaa gtt gaa tgc atg acc tgc aat ggg gag agt tat cga ggt Cys Ser Glu Val Glu Cys Met Thr Cys Asn Gly Glu Ser Tyr Arg Gly 590	595	600	1828
ctc atg gat cat aca gaa tca ggc aag att tgt cag cgc tgg gat cat Leu Met Asp His Thr Glu Ser Gly Lys Ile Cys Gln Arg Trp Asp His 605	610	615	1876
cag aca cca cac cgg cac aaa ttc ttg cct gaa aga tat ccc gac aag Gln Thr Pro His Arg His Lys Phe Leu Pro Glu Arg Tyr Pro Asp Lys 620	625	630	1924
ggc ttt gat gat aat tat tgc cgc aat ccc gat ggc cag ccg agg cca Gly Phe Asp Asp Asn Tyr Cys Arg Asn Pro Asp Gly Gln Pro Arg Pro 635	640	645	1972
tgg tgc tat act ctt gac cct cac acc cgc tgg gag tac tgt gca att Trp Cys Tyr Thr Leu Asp Pro His Thr Arg Trp Glu Tyr Cys Ala Ile 655	660	665	2020
aaa aca tgc gct gac aat act atg aat gac act gat gtt cct ttg gaa Lys Thr Cys Ala Asp Asn Thr Met Asn Asp Thr Asp Val Pro Leu Glu 670	675	680	2068

aca act gaa tgc atc caa ggt caa gga gaa ggc tac agg ggc act gtc	2116
Thr Thr Glu Cys Ile Gln Gly Gln Gly Glu Gly Tyr Arg Gly Thr Val	
685 690 695	
aat acc att tgg aat gga att cca tgt cag cgt tgg gat tct cag tat	2164
Asn Thr Ile Trp Asn Gly Ile Pro Cys Gln Arg Trp Asp Ser Gln Tyr	
700 705 710	
cct cac gag cat gac atg act cct gaa aat ttc aag tgc aag gac cta	2212
Pro His Glu His Asp Met Thr Pro Glu Asn Phe Lys Cys Lys Asp Leu	
715 720 725 730	
cga gaa aat tac tgc cga aat cca gat ggg tct gaa tca ccc tgg tgt	2260
Arg Glu Asn Tyr Cys Arg Asn Pro Asp Gly Ser Glu Ser Pro Trp Cys	
735 740 745	
ttt acc act gat cca aac atc cga gtt ggc tac tgc tcc caa att cca	2308
Phe Thr Thr Asp Pro Asn Ile Arg Val Gly Tyr Cys Ser Gln Ile Pro	
750 755 760	
aac tgt gat atg tca cat gga caa gat tgt tat cgt ggg aat ggc aaa	2356
Asn Cys Asp Met Ser His Gly Gln Asp Cys Tyr Arg Gly Asn Gly Lys	
765 770 775	
aat tat atg ggc aac tta tcc caa aca aga tct gga cta aca tgt tca	2404
Asn Tyr Met Gly Asn Leu Ser Gln Thr Arg Ser Gly Leu Thr Cys Ser	
780 785 790	
atg tgg gac aag aac atg gaa gac tta cat cgt cat atc ttc tgg gaa	2452
Met Trp Asp Lys Asn Met Glu Asp Leu His Arg His Ile Phe Trp Glu	
795 800 805 810	
cca gat gca agt aag ctg aat gag aat tac tgc cga aat cca gat gat	2500
Pro Asp Ala Ser Lys Leu Asn Glu Asn Tyr Cys Arg Asn Pro Asp Asp	
815 820 825	
gat gct cat gga ccc tgg tgc tac acg gga aat cca ctc att cct tgg	2548
Asp Ala His Gly Pro Trp Cys Tyr Thr Gly Asn Pro Leu Ile Pro Trp	
830 835 840	
gat tat tgc cct att tct cgt tgt gaa ggt gat acc aca cct aca ata	2596
Asp Tyr Cys Pro Ile Ser Arg Cys Glu Gly Asp Thr Thr Pro Thr Ile	
845 850 855	
gtc aat tta gac cat ccc gta ata tct tgt gcc aaa acg aaa caa ttg	2644
Val Asn Leu Asp His Pro Val Ile Ser Cys Ala Lys Thr Lys Gln Leu	
860 865 870	
cga gtt gta aat ggg att cca aca cga aca aac ata gga tgg atg gtt	2692
Arg Val Val Asn Gly Ile Pro Thr Arg Thr Asn Ile Gly Trp Met Val	
875 880 885 890	
agt ttg aga tac aga aat aaa cat atc tgc gga gga tca ttg ata aag	2740
Ser Leu Arg Tyr Arg Asn Lys His Ile Cys Gly Gly Ser Leu Ile Lys	
895 900 905	

gag agt tgg gtt ctt act gca cga cag tgt ttc cct tct cgt gac ttg	2788
Glu Ser Trp Val Leu Thr Ala Arg Gln Cys Phe Pro Ser Arg Asp Leu	
910 915 920	
aaa gat tat gaa gct tgg ctt gga att cat gat gtc cac gga aga gga	2836
Lys Asp Tyr Glu Ala Trp Leu Gly Ile His Asp Val His Gly Arg Gly	
925 930 935	
gat gag aaa tgc aaa cag gtt ctc aat gtt tcc cag ctg gta tat ggc	2884
Asp Glu Lys Cys Lys Gln Val Leu Asn Val Ser Gln Leu Val Tyr Gly	
940 945 950	
cct gaa gga tca gat ctg gtt tta atg aag ctt gcc agg cct gct gtc	2932
Pro Glu Gly Ser Asp Leu Val Leu Met Lys Leu Ala Arg Pro Ala Val	
955 960 965 970	
ctg gat gat ttt gtt agt acg att gat tta cct aat tat gga tgc aca	2980
Leu Asp Asp Phe Val Ser Thr Ile Asp Leu Pro Asn Tyr Gly Cys Thr	
975 980 985	
att cct gaa aag acc agt tgc agt gtt tat ggc tgg ggc tac act gga	3028
Ile Pro Glu Lys Thr Ser Cys Ser Val Tyr Gly Trp Gly Tyr Thr Gly	
990 995 1000	
ttg atc aac tat gat ggc cta tta cga gtg gca cat ctc tat ata atg	3076
Leu Ile Asn Tyr Asp Gly Leu Leu Arg Val Ala His Leu Tyr Ile Met	
1005 1010 1015	
gga aat gag aaa tgc agc cag cat cat cga ggg aag gtg act ctg aat	3124
Gly Asn Glu Lys Cys Ser Gln His His Arg Gly Lys Val Thr Leu Asn	
1020 1025 1030	
gag tct gaa ata tgt gct ggg gct gaa aag att gga tca gga cca tgt	3172
Glu Ser Glu Ile Cys Ala Gly Ala Glu Lys Ile Gly Ser Gly Pro Cys	
1035 1040 1045 1050	
gag ggg gat tat ggt ggc cca ctt gtt tgt gag caa cat aaa atg aga	3220
Glu Gly Asp Tyr Gly Gly Pro Leu Val Cys Glu Gln His Lys Met Arg	
1055 1060 1065	
atg gtt ctt ggt gtc att gtt cct ggt cgt gga tgt gcc att cca aat	3268
Met Val Leu Gly Val Ile Val Pro Gly Arg Gly Cys Ala Ile Pro Asn	
1070 1075 1080	
cgt cct ggt att ttt gtc cga gta gca tat tat gca aaa tgg ata cac	3316
Arg Pro Gly Ile Phe Val Arg Val Ala Tyr Tyr Ala Lys Trp Ile His	
1085 1090 1095	
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<210> 20

<211> 1109

<212> PRT

<213> Artificial Sequence

<223> Description of Artificial Sequence:HGF protein fused with HBsAg L protein

<400> 20

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			20					25					30			
Pro	Leu	Gly	Phe	Phe	Pro	Asp	His	Gln	Leu	Asp	Pro	Ala	Phe	Gly	Ala	
		35					40					45				
Asn	Ser	Asn	Asn	Pro	Asp	Trp	Asp	Phe	Asn	Pro	Asn	Lys	Asp	Gln	Trp	
	50					55					60					
Pro	Glu	Ala	Asn	Gln	Val	Gly	Ala	Gly	Ala	Phe	Gly	Pro	Gly	Phe	Thr	
65					70					75					80	
Pro	Pro	His	Gly	Gly	Leu	Leu	Gly	Trp	Ser	Pro	Gln	Ala	Gln	Gly	Ile	
			85						90					95		
Leu	Thr	Thr	Val	Pro	Ala	Ala	Pro	Pro	Pro	Ala	Ser	Thr	Asn	Arg	Gln	
			100					105					110			
Ser	Gly	Arg	Gln	Pro	Thr	Pro	Ile	Ser	Pro	Pro	Leu	Arg	Asp	Ser	His	
	115						120					125				
Pro	Gln	Ala	Met	Gln	Trp	Asn	Ser	Thr	Thr	Phe	His	Gln	Ala	Leu	Leu	
130						135					140					
Asp	Pro	Arg	Val	Arg	Gly	Leu	Tyr	Phe	Pro	Ala	Gly	Gly	Ser	Ser	Ser	
145					150					155					160	
Gly	Thr	Val	Asn	Pro	Val	Pro	Thr	Thr	Ala	Ser	Pro	Ile	Ser	Gly	Asp	
			165						170					175		
Pro	Ala	Pro	Asn	Met	Glu	Asn	Thr	Thr	Ser	Gly	Phe	Leu	Gly	Pro	Leu	
		180						185					190			
Leu	Val	Leu	Gln	Ala	Gly	Phe	Phe	Leu	Leu	Thr	Arg	Ile	Leu	Thr	Ile	
	195						200					205				
Pro	Gln	Ser	Leu	Asp	Ser	Trp	Trp	Thr	Ser	Leu	Asn	Phe	Leu	Gly	Gly	
210						215					220					
Ala	Pro	Thr	Cys	Pro	Gly	Gln	Asn	Ser	Gln	Ser	Pro	Thr	Ser	Asn	His	
225					230					235					240	
Ser	Pro	Thr	Ser	Cys	Pro	Pro	Ile	Cys	Pro	Gly	Tyr	Arg	Trp	Met	Cys	
			245						250					255		
Leu	Arg	Arg	Phe	Ile	Ile	Phe	Leu	Phe	Ile	Leu	Leu	Leu	Cys	Leu	Ile	
		260						265					270			
Phe	Leu	Leu	Val	Leu	Leu	Asp	Tyr	Gln	Gly	Met	Leu	Pro	Val	Cys	Pro	
	275					280						285				
Leu	Leu	Pro	Gly	Thr	Ser	Thr	Thr	Ser	Thr	Gly	Pro	Cys	Lys	Thr	Cys	
290					295					300						
Thr	Ile	Pro	Ala	Gln	Gly	Thr	Ser	Met	Phe	Pro	Ser	Cys	Cys	Cys	Thr	
305				310						315					320	
Lys	Pro	Ser	Asp	Gly	Asn	Cys	Thr	Cys	Ile	Pro	Ile	Pro	Ser	Ser	Trp	
			325						330					335		
Ala	Phe	Ala	Arg	Phe	Leu	Trp	Glu	Trp	Ala	Ser	Val	Arg	Phe	Ser	Trp	
		340					345					350				
Leu	Ser	Leu	Val	Pro	Phe	Val	Gln	Trp	Phe	Val	Gly	Leu	Ser	Pro		
	355					360					365					
Thr	Val	Trp	Leu	Ser	Val	Ile	Trp	Met	Met	Trp	Tyr	Trp	Gly	Pro	Ser	
	370				375						380					
Leu	Tyr	Asn	Ile	Leu	Ser	Pro	Phe	Leu	Pro	Leu	Leu	Pro	Ile	Phe	Phe	
385				390					395						400	
Cys	Leu	Trp	Val	Tyr	Ile	Asp	Tyr	Lys	Asp	Asp	Asp	Asp	Lys	Ile	Pro	
			405						410					415		
Val	Gln	Arg	Lys	Arg	Arg	Asn	Thr	Ile	His	Glu	Phe	Lys	Lys	Ser	Ala	

			420					425					430			
Lys	Thr	Thr	Leu	Ile	Lys	Ile	Asp	Pro	Ala	Leu	Lys	Ile	Lys	Thr	Lys	
		435					440					445				
Lys	Val	Asn	Thr	Ala	Asp	Gln	Cys	Ala	Asn	Arg	Cys	Thr	Arg	Asn	Lys	
	450					455					460					
Gly	Leu	Pro	Phe	Thr	Cys	Lys	Ala	Phe	Val	Phe	Asp	Lys	Ala	Arg	Lys	
465					470					475					480	
Gln	Cys	Leu	Trp	Phe	Pro	Phe	Asn	Ser	Met	Ser	Ser	Gly	Val	Lys	Lys	
			485					490						495		
Glu	Phe	Gly	His	Glu	Phe	Asp	Leu	Tyr	Glu	Asn	Lys	Asp	Tyr	Ile	Arg	
			500					505					510			
Asn	Cys	Ile	Ile	Gly	Lys	Gly	Arg	Ser	Tyr	Lys	Gly	Thr	Val	Ser	Ile	
		515					520					525				
Thr	Lys	Ser	Gly	Ile	Lys	Cys	Gln	Pro	Trp	Ser	Ser	Met	Ile	Pro	His	
	530					535					540					
Glu	His	Ser	Tyr	Arg	Gly	Lys	Asp	Leu	Gln	Glu	Asn	Tyr	Cys	Arg	Asn	
545					550					555					560	
Pro	Arg	Gly	Glu	Glu	Gly	Gly	Pro	Trp	Cys	Phe	Thr	Ser	Asn	Pro	Glu	
				565					570					575		
Val	Arg	Tyr	Glu	Val	Cys	Asp	Ile	Pro	Gln	Cys	Ser	Glu	Val	Glu	Cys	
			580					585					590			
Met	Thr	Cys	Asn	Gly	Glu	Ser	Tyr	Arg	Gly	Leu	Met	Asp	His	Thr	Glu	
		595					600					605				
Ser	Gly	Lys	Ile	Cys	Gln	Arg	Trp	Asp	His	Gln	Thr	Pro	His	Arg	His	
	610				615						620					
Lys	Phe	Leu	Pro	Glu	Arg	Tyr	Pro	Asp	Lys	Gly	Phe	Asp	Asp	Asn	Tyr	
625					630					635					640	
Cys	Arg	Asn	Pro	Asp	Gly	Gln	Pro	Arg	Pro	Trp	Cys	Tyr	Thr	Leu	Asp	
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Pro	His	Thr	Arg	Trp	Glu	Tyr	Cys	Ala	Ile	Lys	Thr	Cys	Ala	Asp	Asn	
			660					665					670			
Thr	Met	Asn	Asp	Thr	Asp	Val	Pro	Leu	Glu	Thr	Thr	Glu	Cys	Ile	Gln	
		675					680					685				
Gly	Gln	Gly	Glu	Gly	Tyr	Arg	Gly	Thr	Val	Asn	Thr	Ile	Trp	Asn	Gly	
	690					695					700					
Ile	Pro	Cys	Gln	Arg	Trp	Asp	Ser	Gln	Tyr	Pro	His	Glu	His	Asp	Met	
705					710					715					720	
Thr	Pro	Glu	Asn	Phe	Lys	Cys	Lys	Asp	Leu	Arg	Glu	Asn	Tyr	Cys	Arg	
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Asn	Pro	Asp	Gly	Ser	Glu	Ser	Pro	Trp	Cys	Phe	Thr	Thr	Asp	Pro	Asn	
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Ile	Arg	Val	Gly	Tyr	Cys	Ser	Gln	Ile	Pro	Asn	Cys	Asp	Met	Ser	His	
		755					760					765				
Gly	Gln	Asp	Cys	Tyr	Arg	Gly	Asn	Gly	Lys	Asn	Tyr	Met	Gly	Asn	Leu	
	770					775					780					

[illegible]